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#2



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RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/09/911,969

TIME: 17:32:58

Input Set : N:\Crf3\RULE60\09911969.txt

Output Set: N:\CRF3\02072002\I911969.raw

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:
7 (i) APPLICANT: Kawamura, Yukio; Morita,
8 Akihiro; Izumo, Koji.; Saka, Tomohide.
10 (ii) TITLE OF INVENTION: ANTITUMOR PROTEIN AND
11 GENE ENCODING SAME
13 (iii) NUMBER OF SEQUENCES: 20
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
17 (B) STREET: 345 PARK AVENUE
18 (C) CITY: NEW YORK
19 (D) STATE: NEW YORK
20 (E) COUNTRY: USA
21 (F) ZIP: 10154
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: FLOPPY DISK
25 (B) COMPUTER: IBM PC COMPATIBLE
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: MICROSOFT WORD 97
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/911,969
C--> 31 (B) FILING DATE: 24-Jul-2001
33 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 09/023,731
36 (B) FILING DATE: 13-FEB-1998
38 (A) APPLICATION NUMBER: JP 29275/1997
39 (B) FILING DATE: 13-FEB-1997
41 (viii) ATTORNEY/AGENT INFORMATION:
42 (A) NAME: KENNETH H. SONNENFELD
43 (B) REGISTRATION NUMBER: 33,285
44 (C) REFERENCE/DOCKET NUMBER: 3479-4000
46 (ix) TELECOMMUNICATION INFORMATION:
47 (A) TELEPHONE: (212) 758-4800
48 (B) TELEFAX: (212) 751-6849
49 (C) TELEX: 421792
51 (2) INFORMATION FOR SEQ ID NO: 1:
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 566
55 (B) TYPE: amino acid
56 (D) TOPOLOGY: linear
58 (ii) MOLECULE TYPE: protein
60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
62 Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg

ENTERED

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```

63   1           5           10           15
65 Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr
66           20           25           30
67 Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg
68           35           40           45
69 His Ile Ile Asp Asn Thr Ser Thr Thr Lys Val Tyr Met Ala Glu Ile
70           50           55           60
71 Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile
72 65           70           75           80
73 Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala
74           85           90           95
75 Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu
76           100          105          110
77 Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu
78           115          120          125
79 Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro
80           130          135          140
81 Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr
82 145          150          155          160
83 Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val
84           165          170          175
85 Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu
86           180          185          190
87 Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val
88           195          200          205
89 Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr
90           210          215          220
91 Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr
92 225          230          235          240
93 Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg
94           245          250          255
95 Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu
96           260          265          270
97 Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr
98           275          280          285
99 Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly
100          290          295          300
101 Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr
102 305          310          315          320
103 Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile
104           325          330          335
105 Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe
106           340          345          350
107 Ala Ala Lys Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu
108           355          360          365
109 Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr
110          370          375          380
111 Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr
112 385          390          395          400

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```

113 Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg
114                               405                               410                               415
115 Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly
116                               420                               425                               430
117 Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr
118                               435                               440                               445
119 Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly
120                               450                               455                               460
122 Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met
123 465                               470                               475                               480
124 Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly
125                               485                               490                               495
126 Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Asp Gln
127                               500                               505                               510
128 Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu
129                               515                               520                               525
130 Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro
131                               530                               535                               540
132 Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val
133 545                               550                               555                               560
134 Asn Tyr Leu Gly Val Ser
135                               565

```

138 (2) INFORMATION FOR SEQ ID NO: 2:

140 (i) SEQUENCE CHARACTERISTICS:

141 (A) LENGTH: 1701

142 (B) TYPE: nucleic acid

C--> 143 (D) TOPOLOGY: linear

144 (D) STRANDNESS: Single

146 (ii) MOLECULE TYPE: cDNA to RNA

148 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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150 ATG CCG ATA CGT CTT TCC AAA GAA AAA ATC AAC GAC CTG CTG CAA CGT48
151 Met Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg
152 1 5 10 15
154 TCT CAA GGG GAT CTT ACT TCC TCG CAA CAC GAA ATT GTA CAT TTC ACT96
155 Ser Gln Gly Asp Leu Thr Ser Ser Gln His Glu Ile Val His Phe Thr
156 20 25 30
158 GAT GTT TTC ATT GCT GGC AGT GGT CCC ATT AGC TGT ACT TAC GCC CGC144
159 Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Ser Cys Thr Tyr Ala Arg
160 35 40 45
162 CAC ATC ATT GAC AAT ACC TCA ACT ACA AAG GTT TAC ATG GCC GAA ATA192
163 His Ile Ile Asp Asn Thr Ser Thr Thr Lys Val Tyr Met Ala Glu Ile
164 50 55 60
166 GGT TCT CAA GAT AAC CCT GTC ATC GGG GCC CAT CAC AAG AAC TCC ATA240
167 Gly Ser Gln Asp Asn Pro Val Ile Gly Ala His His Lys Asn Ser Ile
168 65 70 75 80
170 AAG TTT CAG AAA GAC ATT GAC AAG TTT GTG AAT ATC ATC AAC GGT GCC288
171 Lys Phe Gln Lys Asp Ile Asp Lys Phe Val Asn Ile Ile Asn Gly Ala
172 85 90 95
174 CTC CAG CCG ATT TCG ATT TCG CCA TCG GAC ACC TAC CAG CCC ACT CTC336

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```

175 Leu Gln Pro Ile Ser Ile Ser Pro Ser Asp Thr Tyr Gln Pro Thr Leu
176          100          105          110
179 GCT GTA GCA GCG TGG GCG CCG CCC ATC GAT CCT GCC GAA GGC CAG CTC384
180 Ala Val Ala Ala Trp Ala Pro Pro Ile Asp Pro Ala Glu Gly Gln Leu
181          115          120          125
183 GTG ATT ATG GGA CAC AAT CCG AAT CAG GAG GCC GGC CTG AAC CTT CCC432
184 Val Ile Met Gly His Asn Pro Asn Gln Glu Ala Gly Leu Asn Leu Pro
185          130          135          140
187 GGT AGC GCT GTC ACT AGG ACA GTC GGG GGG ATG GCG ACC CAC TGG ACT480
188 Gly Ser Ala Val Thr Arg Thr Val Gly Gly Met Ala Thr His Trp Thr
189 145          150          155          160
191 TGC GCG TGT CCT ACT CCA CAT GAC GAA GAG AGG GTC AAC AAC CCA GTT528
192 Cys Ala Cys Pro Thr Pro His Asp Glu Glu Arg Val Asn Asn Pro Val
193          165          170          175
195 GAC AAG CAG GAG TTC GAC GCA CTG CTC GAA CGT GCT AAA ACA TTG CTC576
196 Asp Lys Gln Glu Phe Asp Ala Leu Leu Glu Arg Ala Lys Thr Leu Leu
197          180          185          190
199 AAC GTT CAC AGC GAC CAG TAC GAC GAT TCT ATC CGT CAG ATA GTT GTC624
200 Asn Val His Ser Asp Gln Tyr Asp Asp Ser Ile Arg Gln Ile Val Val
201          195          200          205
203 AAA GAG ACT CTT CAG CAG ACC CTT GAT GCG TCG CGG GGT GTG ACC ACT672
204 Lys Glu Thr Leu Gln Gln Thr Leu Asp Ala Ser Arg Gly Val Thr Thr
205          210          215          220
207 CTC CCG CTG GGG GTG GAG CGC CGT ACG GAC AAT CCT ATT TAT GTC ACC720
208 Leu Pro Leu Gly Val Glu Arg Arg Thr Asp Asn Pro Ile Tyr Val Thr
209 225          230          235          240
211 TGG ACC GGT GCC GAT ACC GTC CTT GGT GAT GTG CCG AAG AGT CCC CGA768
212 Trp Thr Gly Ala Asp Thr Val Leu Gly Asp Val Pro Lys Ser Pro Arg
213          245          250          255
215 TTC GCT TTG GTT ACA GAG ACG AGA GTG ACG AAG CTT ATT GTC AGT GAA816
216 Phe Ala Leu Val Thr Glu Thr Arg Val Thr Lys Leu Ile Val Ser Glu
217          260          265          270
219 ACC AAT CCG ACG CAG GTT GTT GCT GCG TTG CTA CGT AAC TTG AAT ACA864
220 Thr Asn Pro Thr Gln Val Val Ala Ala Leu Leu Arg Asn Leu Asn Thr
221          275          280          285
223 AGC AAC GAT GAA CTT GTC GTG GCC AAG AGT TTC GTC ATA GCT TGT GGA912
224 Ser Asn Asp Glu Leu Val Val Ala Lys Ser Phe Val Ile Ala Cys Gly
225          290          295          300
227 GCA GTC TGC ACA CCG CAA ATC TTG TGG AAC AGC AAC ATC CGC CCA TAT960
228 Ala Val Cys Thr Pro Gln Ile Leu Trp Asn Ser Asn Ile Arg Pro Tyr
229 305          310          315          320
231 GCG CTT GGT CGC TAC CTC AGC GAA CAG TCC ATG ACT TTT TGT CAG ATC1008
232 Ala Leu Gly Arg Tyr Leu Ser Glu Gln Ser Met Thr Phe Cys Gln Ile
233          325          330          335
236 GTT CTC AAG AGG GGC ATA GTC GAT GCC ATC GCT ACT GAC CCT CGC TTC1056
237 Val Leu Lys Arg Gly Ile Val Asp Ala Ile Ala Thr Asp Pro Arg Phe
238          340          345          350
240 GCT GCG AAG GTT GAG GCG CAC AAG AAG AAG CAC CCC GAT GAC GTG CTG1104
241 Ala Ala Lys Val Glu Ala His Lys Lys Lys His Pro Asp Asp Val Leu

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PATENT APPLICATION: US/09/911,969

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Input Set : N:\Crf3\RULE60\09911969.txt

Output Set: N:\CRF3\02072002\I911969.raw

```

242          355          360          365
244 CCC ATT CCA TTC CAC GAG CCT GAA CCT CAA GTG ATG ATT CCG TAC ACG1152
245 Pro Ile Pro Phe His Glu Pro Glu Pro Gln Val Met Ile Pro Tyr Thr
246          370          375          380
248 TCG GAC TTC CCT TGG CAT GTT CAG GTG CAT CGC GAT GCA TTC TCA TAT1200
249 Ser Asp Phe Pro Trp His Val Gln Val His Arg Asp Ala Phe Ser Tyr
250 385          390          395          400
252 GGT GAT GTT GGA CCC AAG GCC GAC CCG CGT GTT GTC GTC GAT CTG AGG1248
253 Gly Asp Val Gly Pro Lys Ala Asp Pro Arg Val Val Val Asp Leu Arg
254          405          410          415
256 TTT TTC GGC AAA TCA GAT ATT GTC GAA GAA AAT CGA GTG ACT TTC GGT1296
257 Phe Phe Gly Lys Ser Asp Ile Val Glu Glu Asn Arg Val Thr Phe Gly
258          420          425          430
260 CCG AAC CCT AAG CTA CGC GAG TGG GAA GCG GGT GTT ACA GAC ACT TAT1344
261 Pro Asn Pro Lys Leu Arg Glu Trp Glu Ala Gly Val Thr Asp Thr Tyr
262          435          440          445
264 GGA ATG CCA CAG CCG ACA TTC CAT GTC AAG CGG ACC AAC GCC GAT GGA1392
265 Gly Met Pro Gln Pro Thr Phe His Val Lys Arg Thr Asn Ala Asp Gly
266          450          455          460
268 GAC CGT GAC CAG AGG ATG ATG AAT GAT ATG ACC AAC GTC GCG AAC ATG1440
269 Asp Arg Asp Gln Arg Met Met Asn Asp Met Thr Asn Val Ala Asn Met
270 465          470          475          480
272 CTG GGT GGG TAC CTT CCT GGC TCC TAC CCT CAA TTT ATG GCA CCT GGT1488
273 Leu Gly Gly Tyr Leu Pro Gly Ser Tyr Pro Gln Phe Met Ala Pro Gly
274          485          490          495
276 CTC GTA CTG CAC ATC ACG GGA ACT ACT CGG ATC GGG ACA GAT GAT CAA1536
277 Leu Val Leu His Ile Thr Gly Thr Thr Arg Ile Gly Thr Asp Gln
278          500          505          510
280 ACT TCT GTT GCT GAT CCG ACA TCA AAG GTT CAT AAC TTC AAC AAT CTG1584
281 Thr Ser Val Ala Asp Pro Thr Ser Lys Val His Asn Phe Asn Asn Leu
282          515          520          525
284 TGG GTC GGC GGG AAT GGG TGC ATT CCA GAT GCG ACT GCC TGC AAC CCG1632
285 Trp Val Gly Gly Asn Gly Cys Ile Pro Asp Ala Thr Ala Cys Asn Pro
286          530          535          540
288 ACT CGT ACG AGC GTC GCG TAT GCG CTC AAG GGT GCT GAG GCT GTA GTC1680
289 Thr Arg Thr Ser Val Ala Tyr Ala Leu Lys Gly Ala Glu Ala Val Val
290 545          550          555          560
293 AAT TAC CTT GGC GTC TCC TGA          1701
294 Asn Tyr Leu Gly Val Ser *
295          565
298 (2) INFORMATION FOR SEQ ID NO: 3:
300 (i) SEQUENCE CHARACTERISTICS:
301 (A) LENGTH: 29
302 (B) TYPE: amino acid
303 (D) TOPOLOGY: linear
305 (ii) MOLECULE TYPE: peptide
307 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
309 Pro Ile Arg Leu Ser Lys Glu Lys Ile Asn Asp Leu Leu Gln Arg Ser
310 1 5 10 15

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/911,969

DATE: 02/07/2002

TIME: 17:32:59

Input Set : N:\Crf3\RULE60\09911969.txt

Output Set: N:\CRF3\02072002\I911969.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:143 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
L:606 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19
L:621 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20